

SEQUENCE LISTING



<110> Scott, Fred

<120> Recombinant Multivalent Viral Vaccine

<130> 18617.0016

<140> US 09/873,881

<141> 2001-06-04

<150> US 08/552,369

<151> 1995-11-03

<160> 19

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Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly	
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ggt ggt ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc	135
Gly Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe	
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aat aat cag acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa	180
Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu	
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atc aca gca aac tca agc aga ctt gta cat tta aat atg cca gaa	225
Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu	
65 70 75	
agt gaa aat tat aaa aga gta gtt gta aat aat atg gat aaa act	270
Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr	
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gca gtt aaa gga aac atg gct tta gat gac act cat gta caa att	315
Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile	
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gta aca cct tgg tca ttg gtt gat gca aat gct tgg gga gtt tgg	360
Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp	
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Lys	Thr	Val	Ser	Glu	Ser	Ala	Thr	Gln	Pro	Pro	Thr	Lys	Val	Tyr	
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Asp	Pro	Asp	Ala	Ser	Ala	Asn	Met	Ser	Arg	Ile	Val	Thr	Tyr	Ser	
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Cys	Pro	Asn	Asn	Leu	Val	Val	Glu	Asp	Glu	Gly	Cys	Thr	Asn	
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Leu	Ser	Gly	Phe	Ser	Tyr	Met	Glu	Leu	Lys	Val	Gly	Tyr	Ile	
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Thr	Glu	Ala	Glu	Thr	Tyr	Thr	Asn	Phe	Val	Gly	Tyr	Val	Thr	
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acc	acg	ttc	aaa	aga	aag	cat	ttc	cgc	cca	aca	cca	gat	gca	336
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Cys	Arg	Ala	Ala	Tyr	Asn	Trp	Lys	Met	Ala	Gly	Asp	Pro	Arg	
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Tyr	Glu	Glu	Ser	Leu	His	Asn	Pro	Tyr	Pro	Asp	Tyr	Arg	Trp	
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ctt	cga	act	gta	aaa	acc	acc	aag	gag	tct	ctc	gtt	atc	ata	462
Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile	
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Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu	
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Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile	
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Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile	
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Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu	

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Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu														
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Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn														
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gac	ttt	cgc	tca	gac	gaa	att	gag	cac	ctt	gtt	gta	gag	gag														882
Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu														
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Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His														
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tta	aga	aaa	ctt	gtc	cct	ggg	ttt	gga	aaa	gca	tat	acc	ata														1008
Leu	Arg	Lys	Leu	Val	Pro	Gly	Phe	Gly	Lys	Ala	Tyr	Thr	Ile														
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Phe	Asn	Lys	Thr	Leu	Met	Glu	Ala	Asp	Ala	His	Tyr	Lys	Ser														
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Val	Arg	Thr	Trp	Asn	Glu	Ile	Leu	Pro	Ser	Lys	Gly	Cys	Leu														
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Arg	Val	Gly	Gly	Arg	Cys	His	Pro	His	Val	Asn	Gly	Val	Phe														
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Pro	Glu	Met	Gln	Ser	Ser	Leu	Leu	Gln	Gln	His	Met	Glu	Leu														
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Leu	Glu	Ser	Ser	Val	Ile	Pro	Leu	Val	His	Pro	Leu	Ala	Asp	
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Val	Glu	Val	His	Leu	Pro	Asp	Val	His	Asn	Gln	Val	Ser	Gly	
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Val	Asp	Leu	Gly	Leu	Pro	Asn	Trp	Gly	Lys	Tyr		Val	Leu	
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Met	Thr	Cys	Cys	Arg	Arg	Val	Asn	Arg	Ser	Glu	Pro	Thr	Gln	
			480					485					490	
cac	aat	ctc	aga	ggg	aca	ggg	agg	gag	gtg	tca	gtc	act	ccc	1512
His	Asn	Leu	Arg	Gly	Thr	Gly	Arg	Glu	Val	Ser	Val	Thr	Pro	
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caa	agc	ggg	aag	atc	ata	tct	tca	tgg	gaa	tca	cac	aag	agt	1554
Gln	Ser	Gly	Lys	Ile	Ile	Ser	Ser	Trp	Glu	Ser	His	Lys	Ser	
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Pro	His	Ile	Lys	Leu	Val	Ile	Asn	Pro	Asn	Lys	Phe	Leu	His	Val	
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Gly	Phe	Cys	Asp	Asn	Pro	Leu	Met	Cys	Cys	Tyr	Pro	Glu	Leu	Leu	
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cct	gaa	ttt	ggc	acc	atg	tgg	gat	tgt	gat	caa	tcg	cca	ctc	caa	180
Pro	Glu	Phe	Gly	Thr	Met	Trp	Asp	Cys	Asp	Gln	Ser	Pro	Leu	Gln	

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gtc	tac	ctt	gag	tca	atc	ctg	ggg	gat	gat	gaa	tgg	tcc	tcc	act	225					
Val	Tyr	Leu	Glu	Ser	Ile	Leu	Gly	Asp	Asp	Glu	Trp	Ser	Ser	Thr						
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cat	gaa	gca	att	gac	cca	gtt	gtg	cca	cca	atg	cat	tgg	gat	gaa	270					
His	Glu	Ala	Ile	Asp	Pro	Val	Val	Pro	Pro	Met	His	Trp	Asp	Glu						
				80					85					90						
gcc	gga	aaa	atc	ttc	caa	cca	cac	cct	ggc	gtc	ctt	atg	cat	cac	315					
Ala	Gly	Lys	Ile	Phe	Gln	Pro	His	Pro	Gly	Val	Leu	Met	His	His						
				95					100					105						
ctc	atc	tgt	aag	gtt	gca	gaa	gga	tgg	gac	cca	aac	ctg	cca	ctt	360					
Leu	Ile	Cys	Lys	Val	Ala	Glu	Gly	Trp	Asp	Pro	Asn	Leu	Pro	Leu						
				110					115					120						
ttc	cgc	ttg	gaa	gcg	gac	gat	ggg	tcc	atc	acg	aca	cct	gaa	cag	405					
Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln						
				125					130					135						
gga	aca	atg	gtt	ggg	gga	gtc	att	gct	gag	ccc	aac	gcc	caa	atg	450					
Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met						
				140					145					150						
tca	acc	gca	gct	gac	atg	gcc	act	ggg	aaa	agt	gtg	gac	tct	gag	495					
Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu						
				155					160					165						
tgg	gaa	gcc	ttc	ttc	tcc	ttt	cac	act	agt	gtg	aac	tgg	agc	aca	540					
Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr						
				170					175					180						
tct	gaa	act	cag	ggg	aag	ata	ctc	ttt	aaa	caa	tcc	tta	gga	cca	585					
Ser	Glu	Thr	Gln	Gly	Lys	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro						
				185					190					195						
ttg	ctc	aac	ccc	tac	ctt	acc	cat	ctt	gca	aag	ctg	tat	gtt	gct	630					
Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala						
				200					205					210						
tgg	tct	ggg	tct	gtt	gat	gtt	agg	ttt	tct	att	tct	gga	tct	ggg	675					
Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly						
				215					220					225						
gtc	ttt	gga	ggg	aaa	tta	gct	gct	att	gtt	gtg	ccg	cca	gga	att	720					
Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile						
				230					235					240						
gat	cct	gtt	caa	agt	act	tca	atg	ctg	caa	tat	cct	cat	gtc	ctc	765					
Asp	Pro	Val	Gln	Ser	Thr	Ser	Met	Leu	Gln	Tyr	Pro	His	Val	Leu						
				245					250					255						
ttt	gat	gct	cgt	caa	gtt	gaa	cct	gtt	atc	ttt	tcc	att	ccc	gat	810					

Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	
				260					265					270	
cta	aga	agc	acc	tta	tat	cac	ctt	atg	tct	gac	act	gat	acc	aca	855
Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	
				275					280					285	
tcg	ttg	gta	atc	atg	gtg	tac	aat	gat	ctt	att	aac	ccc	tat	gct	900
Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	
				290					295					300	
aat	gac	tca	aac	tct	tcg	ggc	tgc	att	gtc	act	gtg	gaa	act	aaa	945
Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	
				305					310					315	
ccg	ggg	cca	gat	ttc	aag	ttt	cac	ctc	tta	aaa	cct	cct	ggg	tct	990
Pro	Gly	Pro	Asp	Phe	Lys	Phe	His	Leu	Leu	Lys	Pro	Pro	Gly	Ser	
				320					325					330	
atg	tta	act	cac	gga	tct	atc	cca	tct	gat	cta	atc	cca	aaa	tca	1035
Met	Leu	Thr	His	Gly	Ser	Ile	Pro	Ser	Asp	Leu	Ile	Pro	Lys	Ser	
				335					340					345	
tct	tcg	ctt	tgg	att	gga	aat	cgg	ttt	tgg	tct	gac	ata	acc	gat	1080
Ser	Ser	Leu	Trp	Ile	Gly	Asn	Arg	Phe	Trp	Ser	Asp	Ile	Thr	Asp	
				350					355					360	
ttt	gta	att	cgg	cct	ttt	gtg	ttc	cag	gca	aat	cga	cac	ttt	gat	1125
Phe	Val	Ile	Arg	Pro	Phe	Val	Phe	Gln	Ala	Asn	Arg	His	Phe	Asp	
				365					370					375	
ttc	aac	caa	gag	aca	gca	ggg	tgg	agc	acc	cca	agg	ttt	cgc	cca	1170
Phe	Asn	Gln	Glu	Thr	Ala	Gly	Trp	Ser	Thr	Pro	Arg	Phe	Arg	Pro	
				380					385					390	
att	act	atc	act	atc	agt	gtt	aag	gag	tca	gca	aag	ctt	ggg	att	1215
Ile	Thr	Ile	Thr	Ile	Ser	Val	Lys	Glu	Ser	Ala	Lys	Leu	Gly	Ile	
				395					400					405	
gga	gtg	gcc	acc	gac	tac	att	gtt	ccc	ggc	ata	cca	gat	gga	tgg	1260
Gly	Val	Ala	Thr	Asp	Tyr	Ile	Val	Pro	Gly	Ile	Pro	Asp	Gly	Trp	
				410					415					420	
ccc	gac	aca	aca	atc	cca	ggg	gag	ttg	gta	cct	gtt	ggg	gac	tat	1305
Pro	Asp	Thr	Thr	Ile	Pro	Gly	Glu	Leu	Val	Pro	Val	Gly	Asp	Tyr	
				425					430					435	
gcc	atc	act	aat	ggc	acc	aac	aat	gat	atc	acc	aca	gct	gcg	cag	1350
Ala	Ile	Thr	Asn	Gly	Thr	Asn	Asn	Asp	Ile	Thr	Thr	Ala	Ala	Gln	
				440					445					450	
tac	gat	gca	gcc	act	gag	att	aga	aac	aac	acc	aat	ttc	aga	ggc	1395
Tyr	Asp	Ala	Ala	Thr	Glu	Ile	Arg	Asn	Asn	Thr	Asn	Phe	Arg	Gly	
				455					460					465	

atg	tac	att	tgt	ggt	tct	ctt	caa	aga	gct	tgg	ggg	gat	aag	aag	1440
Met	Tyr	Ile	Cys	Gly	Ser	Leu	Gln	Arg	Ala	Trp	Gly	Asp	Lys	Lys	
				470					475					480	
att	tca	aat	act	gct	ttt	atc	aca	acc	ggc	acg	gtt	gat	gga	gcc	1485
Ile	Ser	Asn	Thr	Ala	Phe	Ile	Thr	Thr	Gly	Thr	Val	Asp	Gly	Ala	
				485					490					495	
aaa	ttg	ata	ccc	agt	aat	acc	att	gac	caa	aca	aaa	att	gcc	gta	1530
Lys	Leu	Ile	Pro	Ser	Asn	Thr	Ile	Asp	Gln	Thr	Lys	Ile	Ala	Val	
				500					505					510	
ttc	caa	gac	aca	cat	gcg	aat	aag	cat	gtc	cag	acc	tcg	gac	gac	1575
Phe	Gln	Asp	Thr	His	Ala	Asn	Lys	His	Val	Gln	Thr	Ser	Asp	Asp	
				515					520					525	
aca	ttg	gcc	ctg	ctt	ggt	tat	act	ggt	att	ggt	gag	gaa	gca	att	1620
Thr	Leu	Ala	Leu	Leu	Gly	Tyr	Thr	Gly	Ile	Gly	Glu	Glu	Ala	Ile	
				530					535					540	
ggt	gct	gac	cgc	gat	aga	gtt	gtg	cga	att	agc	gtc	ctc	ccg	gaa	1665
Gly	Ala	Asp	Arg	Asp	Arg	Val	Val	Arg	Ile	Ser	Val	Leu	Pro	Glu	
				545					550					555	
cgt	ggc	gca	cgt	ggt	ggc	aat	cac	cca	atc	ttc	cac	aaa	aac	tct	1710
Arg	Gly	Ala	Arg	Gly	Gly	Asn	His	Pro	Ile	Phe	His	Lys	Asn	Ser	
				560					565					570	
atc	aag	ctt	ggt	tat	gta	att	agg	tcc	att	gat	gtg	ttc	aat	tct	1755
Ile	Lys	Leu	Gly	Tyr	Val	Ile	Arg	Ser	Ile	Asp	Val	Phe	Asn	Ser	
				575					580					585	
caa	att	ctg	cat	acc	tct	agg	caa	ctt	tcc	ctc	aat	cat	tac	tta	1800
Gln	Ile	Leu	His	Thr	Ser	Arg	Gln	Leu	Ser	Leu	Asn	His	Tyr	Leu	
				590					595					600	
ttg	tcg	cct	gac	tcc	ttt	gct	gtc	tat	agg	att	att	gac	tct	aat	1845
Leu	Ser	Pro	Asp	Ser	Phe	Ala	Val	Tyr	Arg	Ile	Ile	Asp	Ser	Asn	
				605					610					615	
gga	tcc	tgg	ttt	gac	ata	ggc	att	gat	aat	gat	gga	ttt	tct	ttt	1890
Gly	Ser	Trp	Phe	Asp	Ile	Gly	Ile	Asp	Asn	Asp	Gly	Phe	Ser	Phe	
				620					625					630	
gtt	ggt	gta	tca	agt	att	ggt	aaa	tta	gag	ttt	cct	tta	act	gcc	1935
Val	Gly	Val	Ser	Ser	Ile	Gly	Lys	Leu	Glu	Phe	Pro	Leu	Thr	Ala	
				635					640					645	
tcc	tac	atg	gga	att	caa	ttg	gca	aaa	att	cga	ctt	gcc	tct	aac	1980
Ser	Tyr	Met	Gly	Ile	Gln	Leu	Ala	Lys	Ile	Arg	Leu	Ala	Ser	Asn	
				650					655					660	
att	agg	agt	gtg	atg	aca	aaa	tta	tga							2007
Ile	Arg	Ser	Val	Met	Thr	Lys	Leu								
				665											

<210> 8
 <211> 582
 <212> DNA
 <213> artificial sequence

<220>
 <223> hemagglutinin left arm

<400> 8
 attaaacgca aatatccatg gaaaacgcgc agtatacaga cgattttttta 50
 cagtattttgg agagtttttat aggaagtata tagagtagaa ccagaatttt 100
 gtaaaaataa atcacatttt tataactaata tgaacaact atcgatagtt 150
 atattgctac tatcgatagt atatacaacc aaacctcatc ctacacagat 200
 atcaaaaaaa ctaggcgatg atgctactct atcgtgtaat agaaacaata 250
 cacatggata tcttgctcatg agttcttggt ataagaaacc agactccatt 300
 attctcttag cagccaaaaa cgatgtcgtg tactttgatg attatacagc 350
 ggataaagta tcatacgatt caccgatga tactctagct acaattatta 400
 caattaaatc attgacatct gcagatgcag gtacttatat atgcgcattc 450
 ttataaacat caacaaatga tacggataaa atagattatg aagaatactt 500
 catagatttg gttgtaaatc cagctaattgt atccactatt gacgcgattc 550
 tatcaggatc taattttctcc gtgataggta tc 582

<210> 9
 <211> 447
 <212> DNA
 <213> artificial sequence

<220>
 <223> hemagglutinin right arm

<400> 9
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 atgaaccaat atctgtatca tcctcgatac caacaacggt agaaagtgtt 100
 acaatatcta ctacaaaata tacaactagt gactttatag agatatttgg 150
 cattgtttca ctaattttat tattggcgtt ggcgattttc tgtattatat 200
 tattttctgta gtggacggtc tcgtaaacaa gaaacaaata tattatagat 250
 tttaactcag ataaatgtct ggaataatta aatctatcgt tttgagcgga 300
 ccatctgggt ccggcaagac agctatagtc aggagactct tacaagatta 350
 tggaaatata tttggatttg tggtatccca taccactaga tttcctcgtc 400
 ctatggaacg agaaggtgtc gactaccatt acgttaacag agaggcc 447

<210> 10
 <211> 40
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer P3

<400> 10
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<210> 11
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<220>
<223> primer P1

<400> 11
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<210> 12
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> primer F2

<400> 12
gcggtaccct ggggttaggc gatagag 27

<210> 13
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer P5

<400> 13
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<210> 14
<211> 22
<212> DNA
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<220>
<223> primer P5

<400> 14
ggcctctctg ttaacgtaat gg 22

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<211> 22
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<220>
<223> primer P2

<400> 15
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<210> 16
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<212> DNA
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<220>
<223> primer P4

<400> 16
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<210> 17
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<212> DNA
<213> feline infectious peritonitis virus

<220>
<223>

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atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96
Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
1 5 10 15

tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
20 25 30

att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
35 40 45

gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
50 55 60

ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
65 70 75

ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta 321
Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
80 85 90

tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct 366
Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
95 100 105

gag	tac	caa	gtt	tcc	aga	tat	gta	atg	ttc	ggc	ttt	agt	gtt	gca	411
Glu	Tyr	Gln	Val	Ser	Arg	Tyr	Val	Met	Phe	Gly	Phe	Ser	Val	Ala	120
				110					115						
ggt	gca	gtt	gta	acg	ttt	gca	ctt	tgg	atg	atg	tat	ttt	gtg	aga	456
Gly	Ala	Val	Val	Thr	Phe	Ala	Leu	Trp	Met	Met	Tyr	Phe	Val	Arg	135
				125					130						
tct	gtt	cag	cta	tat	aga	aga	acc	aaa	tca	tgg	tgg	tct	ttt	aat	501
Ser	Val	Gln	Leu	Tyr	Arg	Arg	Thr	Lys	Ser	Trp	Trp	Ser	Phe	Asn	150
				140					145						
cct	gag	act	aat	gca	att	ctt	tgt	gtt	aat	gca	ttg	ggt	aga	agt	546
Pro	Glu	Thr	Asn	Ala	Ile	Leu	Cys	Val	Asn	Ala	Leu	Gly	Arg	Ser	165
				155					160						
tat	gtg	ctt	ccc	tta	gat	ggt	act	cct	aca	ggt	gtt	acc	ctt	act	591
Tyr	Val	Leu	Pro	Leu	Asp	Gly	Thr	Pro	Thr	Gly	Val	Thr	Leu	Thr	180
				170					175						
cta	ctt	tca	gga	aat	cta	tat	gct	gaa	ggt	ttc	aaa	atg	gct	ggt	636
Leu	Leu	Ser	Gly	Asn	Leu	Tyr	Ala	Glu	Gly	Phe	Lys	Met	Ala	Gly	195
				185					190						
ggt	tta	acc	atc	gag	cat	ttg	cct	aaa	tac	gtc	atg	att	gct	aca	681
Gly	Leu	Thr	Ile	Glu	His	Leu	Pro	Lys	Tyr	Val	Met	Ile	Ala	Thr	210
				200					205						
cct	agt	aga	acc	atc	gtt	tat	aca	tta	gtt	gga	aaa	caa	tta	aaa	726
Pro	Ser	Arg	Thr	Ile	Val	Tyr	Thr	Ile	Val	Gly	Lys	Gln	Leu	Lys	225
				215					220						
gca	act	act	gcc	aca	gga	tgg	gct	tac	tac	gta	aaa	tct	aaa	gct	771
Ala	Thr	Thr	Ala	Thr	Gly	Trp	Ala	Tyr	Tyr	Val	Lys	Ser	Lys	Ala	240
				230					235						
ggt	gat	tac	tca	aca	gaa	gca	cgt	act	gac	aat	ttg	agt	gaa	cat	816
Gly	Asp	Tyr	Ser	Thr	Glu	Ala	Arg	Thr	Asp	Asn	Leu	Ser	Glu	His	255
				245					250						
gaa	aaa	tta	tta	cat	atg	gtg	taa								840
Glu	Lys	Leu	Leu	His	Met	Val									
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<210> 18

<211> 1144

<212> DNA

<213> feline infectious peritonitis virus

<220>

<223>

<400> 18

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Met	Ala	Thr	Gln	Gly	Gln	Arg	Val	Asn	Trp	Gly	Asp	Glu	Pro	Ser	
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aaa	aga	cgt	ggt	cgt	tct	aac	tct	cgt	ggt	cgg	aag	aat	aat	gat	90
Lys	Arg	Arg	Gly	Arg	Ser	Asn	Ser	Arg	Gly	Arg	Lys	Asn	Asn	Asp	
				20					25					30	
ata	cct	ttg	tca	ttc	tac	aac	ccc	att	acc	ctc	gaa	caa	gga	tct	135
Ile	Pro	Leu	Ser	Phe	Tyr	Asn	Phe	Ile	Thr	Leu	Glu	Gln	Glu	Ser	
				35					40					45	
aaa	ttt	tgg	aat	tta	tgt	ccg	aga	gac	ctt	gtt	ccc	aaa	gga	ata	180
Lys	Phe	Trp	Asn	Leu	Cys	Pro	Arg	Asp	Leu	Val	Pro	Lys	Gly	Ile	
				50					55					60	
ggt	aat	aag	gat	caa	caa	att	ggt	tat	tgg	aat	aga	cag	att	cgt	225
Gly	Asn	Lys	Asp	Gln	Gln	Ile	Gly	Tyr	Trp	Asn	Arg	Gln	Ile	Arg	
				65					70					75	
tat	cgt	att	gta	aaa	ggc	cag	cgt	aag	gaa	ctc	gct	gag	agg	tgg	270
Tyr	Arg	Ile	Val	Lys	Gly	Gln	Arg	Lys	Glu	Leu	Ala	Glu	Arg	Trp	
				80					85					90	
ttc	ttt	tac	ttc	tta	ggt	aca	gga	cct	cat	gct	gat	gct	aaa	ttc	315
Phe	Phe	Tyr	Phe	Leu	Gly	Thr	Gly	Phe	His	Ala	Asp	Ala	Lys	Phe	
				95					100					105	
aaa	gac	aag	att	gat	gga	gtc	ttc	tgg	gtt	gca	agg	gat	ggt	gcc	360
Lys	Asp	Lys	Ile	Asp	Gly	Val	Phe	Trp	Val	Ala	Arg	Asp	Gly	Ala	
				110					115					120	
atg	aac	aag	ccc	aca	acg	ctt	ggc	act	cgt	gga	acc	aat	aac	gaa	405
Met	Asn	Lys	Pro	Thr	Thr	Leu	Gly	Thr	Arg	Gly	Thr	Asn	Asn	Glu	
				125					130					135	
tcc	aaa	cca	ctg	aga	ttt	gat	ggt	aag	ata	ccg	cca	cag	ttt	cag	450
Ser	Lys	Pro	Leu	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Pro	Gln	Phe	Gln	
				140					145					150	
ctt	gaa	gtg	aac	cgt	tct	agg	aac	aat	tca	agg	tct	ggt	tct	cag	495
Leu	Glu	Val	Asn	Arg	Ser	Arg	Asn	Asn	Ser	Arg	Ser	Gly	Ser	Gln	
				155					160					165	
tct	aga	tct	gtt	tca	aga	aac	aga	tct	caa	tct	aga	gga	aga	cac	540
Ser	Arg	Ser	Val	Ser	Arg	Asn	Arg	Ser	Gln	Ser	Arg	Gly	Arg	His	
				170					175					180	
cat	tcc	aat	aac	cag	aat	aat	aat	gtt	gag	gat	aca	att	gta	gcc	585
His	Ser	Asn	Asn	Gln	Asn	Asn	Asn	Val	Glu	Asp	Thr	Ile	Val	Ala	
				185					190					195	
gtg	ctt	gaa	aaa	tta	ggt	gtt	act	gac	aaa	caa	agg	tca	cgt	tct	630
Val	Leu	Glu	Lys	Leu	Gly	Val	Thr	Asp	Lys	Gln	Arg	Ser	Arg	Ser	
				200					205					210	

aaa cct aga gaa cgt agt gat tcc aaa cct agg gac aca aca cct	675
Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro	225
215	
aag aat gcc aac aaa cac acc tgg aag aaa act gca ggc aag gga	720
Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly	240
230	
235	
gat gtg aca act ttc tat ggt gct aga agt agt tca gct aac ttt	765
Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe	255
245	
250	
ggg gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac	810
Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr	270
260	
265	
cct cag ata gct gaa tgt gtt cca tca gtg tct agc ata atc ttt	855
Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe	285
275	
280	
ggc agt caa tgg tct gct gaa gaa gct ggt gat caa gtg aaa gtc	900
Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val	300
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295	
acg ctc act cac acc tac tac ctg cca aag gat gat gcc aaa act	945
Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr	315
305	
310	
agt caa ttc cta gaa cag att gac gct tac aag cga cct tct gaa	990
Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu	330
320	
325	
gtg gct aag gat cag agg caa aga aga tcc cgt tct aag tct gct	1035
Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala	345
335	
340	
gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	1080
Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	360
350	
355	
aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt	1125
Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val	375
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Thr Asn	

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<212> DNA

<213> feline leukemia virus

<220>

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Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu	
1 5 10 15	
tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac	140
Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp	
20 25 30	
ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act	185
Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr	
35 40 45	
tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc	230
Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr	
50 55 60	
tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt	275
Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val	
65 70 75	
gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta	320
Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu	
80 85 90	
aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa	365
Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys	
95 100 105	
tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac	410
Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr	
110 115 120	
ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag	455
Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys	
125 130 135	
gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	500
Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp	
140 145 150	
gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca	545
Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser	
155 160 165	
tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc	590
Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser	
170 175 180	
tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag	635
Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys	

	185	190	195	
	gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga			680
	Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg			
	200	205	210	
	cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc			725
	Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser			
	215	220	225	
	cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac			770
	Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn			
	230	235	240	
	cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca			815
	Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr			
	245	250	255	
	ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc			860
	Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala			
	260	265	270	
	cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg			905
	Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly			
	275	280	285	
	acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc			950
	Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala			
	290	295	300	
	tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc			995
	Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys			
	305	310	315	
	ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt			1040
	Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly			
	320	325	330	
	acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act			1085
	Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile			
	335	340	345	
	ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg			1130
	Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met			
	350	355	360	
	tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag			1175
	Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys			
	365	370	375	
	aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac			1220
	Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn			
	380	385	390	
	ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc			1265

Gly	Thr	Tyr	Trp	Ala	Cys	Asn	Thr	Gly	Leu	Thr	Pro	Cys	Ile	Ser	
				395					400					405	
atg	gcg	gtg	ctc	aat	tgg	acc	tct	gat	ttt	tgt	gtc	tta	atc	gaa	1310
Met	Ala	Val	Leu	Asn	Trp	Thr	Ser	Asp	Phe	Cys	Val	Leu	Ile	Glu	
				410					415					420	
tta	tgg	ccc	aga	gtg	act	tac	cat	caa	ccc	gaa	tat	gtg	tac	aca	1355
Leu	Trp	Pro	Arg	Val	Thr	Tyr	His	Gln	Pro	Glu	Tyr	Val	Tyr	Thr	
				425					430					435	
cat	ttt	gcc	aaa	gct	gtc	agg	ttc	cga	aga	gaa	cca	ata	tca	cta	1400
His	Phe	Ala	Lys	Ala	Val	Arg	Phe	Arg	Arg	Glu	Pro	Ile	Ser	Leu	
				440					445					450	
acg	gtt	gcc	ctt	atg	ttg	gga	gga	ctt	act	gta	ggg	ggc	ata	gcc	1445
Thr	Val	Ala	Leu	Met	Leu	Gly	Gly	Leu	Thr	Val	Gly	Gly	Ile	Ala	
				455					460					465	
gcg	ggg	gtc	gga	aca	ggg	act	aaa	gcc	ctc	ctt	gaa	aca	gcc	cag	1490
Ala	Gly	Val	Gly	Thr	Gly	Thr	Lys	Ala	Leu	Leu	Glu	Thr	Ala	Gln	
				470					475					480	
ttc	aga	caa	cta	caa	atg	gcc	atg	cac	aca	gac	atc	cag	gcc	cta	1535
Phe	Arg	Gln	Leu	Gln	Met	Ala	Met	His	Thr	Asp	Ile	Gln	Ala	Leu	
				485					490					495	
gaa	gaa	tca	att	agt	gcc	tta	gaa	aag	tcc	ctg	acc	tcc	ctt	tct	1580
Glu	Glu	Ser	Ile	Ser	Ala	Leu	Glu	Lys	Ser	Leu	Thr	Ser	Leu	Ser	
				500					505					510	
gaa	gta	gtc	tta	caa	aac	aga	cgg	ggc	cta	gat	att	cta	ttc	tta	1625
Glu	Val	Val	Leu	Gln	Asn	Arg	Arg	Glu	Leu	Asp	Ile	Leu	Phe	Leu	
				515					520					525	
caa	gag	gga	ggg	ctc	tgt	gcc	gca	ttg	aaa	gaa	gaa	tgt	tgc	ttc	1670
Gln	Glu	Gly	Gly	Leu	Cys	Ala	Ala	Leu	Lys	Glu	Glu	Cys	Cys	Phe	
				530					535					540	
tat	gcg	gat	cac	acc	gga	ctc	gtc	cga	gac	aat	atg	gcc	aaa	tta	1715
Tyr	Ala	Asp	His	Thr	Gly	Leu	Val	Arg	Asp	Asn	Met	Ala	Lys	Leu	
				545					550					555	
aga	gaa	aga	cta	aaa	cag	cgg	caa	caa	ctg	ttt	gac	tcc	caa	cag	1760
Arg	Glu	Arg	Leu	Lys	Gln	Arg	Gln	Gln	Leu	Phe	Asp	Ser	Gln	Gln	
				560					565					570	
gga	tgg	ttt	gaa	gga	tgg	ttc	aac	aag	tcc	ccc	tgg	ttt	aca	acc	1805
Gly	Trp	Phe	Glu	Gly	Trp	Phe	Asn	Lys	Ser	Pro	Trp	Phe	Thr	Thr	
				575					580					585	
cta	att	tcc	tcc	att	atg	ggc	ccc	tta	cta	atc	cta	ctc	cta	att	1850
Leu	Ile	Ser	Ser	Ile	Met	Gly	Pro	Leu	Leu	Ile	Leu	Leu	Leu	Ile	
				590					595					600	

ctc	ctc	ttc	ggc	cca	tgc	atc	ctt	aac	cga	tta	gta	caa	ttc	gta	1895
Leu	Leu	Phe	Gly	Pro	Cys	Ile	Leu	Asn	Arg	Leu	Val	Gln	Phe	Val	
				605					610					615	
aaa	gac	aga	ata	tct	gtg	gta	cag	gct	tta	att	tta	acc	caa	cag	1940
Lys	Asp	Axg	Ile	Ser	Val	Val	Gln	Ala	Leu	Ile	Leu	Thr	Gln	Gln	
				620					625					630	
tac	caa	cag	ata	aag	caa	tac	gat	ccg	gac	cga	cca	tga			1979
Tyr	Gln	Gln	Ile	Lys	Gln	Tyr	Asp	Pro	Asp	Arg	Pro				
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